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Petrus J.T. Dekker
Marco A. van den Berg

<120> FILAMENTOUS FUNGAL MUTANTS WITH IMPROVED HOMOLOGOUS RECOMBINATION EFFICIENCY

<130> 3663-335 / 24181USWO

<140> US

<141> 2006-09-25

<150> PCT/EP2005/051464

<151> 2005-03-31

<150> EP 04076057.1

<151> 2004-04-02

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Cys Ala Tyr His Phe Met Gln Gln Arg Ile Ile Ser Asn Pro Gln Asp
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<213> *Aspergillus niger*

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<213> *Aspergillus niger*

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Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr	
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Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala	
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Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly	
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Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile	
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Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly	
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Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu	
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 225 230 235 240
 Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
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 Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
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 Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
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<212> DNA

<213> *Aspergillus niger*

<220>

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Trp	Ile	Thr	Pro	Val	Thr	Ala	Gln	Leu	Pro	Gln	Thr	Thr	Ala	Tyr	Gly	
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Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly	
130 135 140	
tat gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc	480
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe	
145 150 155 160	
agt tcc caa gac tac ttc cac ccg ttc tgt ttc att caa aac tat gaa	528
Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu	
165 170 175	
gat cag act cag gtt gag gat tgc tgg cta gga gat aac act gtc tcc	576
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser	
180 185 190	
ttg cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac	624
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr	
195 200 205	
gac tgg gtg gga tca ttg gta tgc aac tac tcc att gac ggc ctc cgt	672
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg	
210 215 220	
atc gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac	720
Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn	
225 230 235 240	
aaa gcc gca ggc gtg tac tgt atc gcc gag gtg ctc gac ggt gat ccg	768
Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro	
245 250 255	
gcc tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat	816
Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr	
260 265 270	
ccc att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc	864
Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser	
275 280 285	
atg gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca	912
Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro	
290 295 300	
gac tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cgg	960
Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg	
305 310 315 320	
ttc gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca	1008
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala	
325 330 335	

ttc atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa	1056
Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu	
340 345 350	
cag cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg	1104
Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp	
355 360 365	
ctc tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc	1152
Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser	
370 375 380	
gcg aac gca atc cgg aac tat gcc att agc aaa gat aca gga ttc gtg	1200
Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val	
385 390 395 400	
acc tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg	1248
Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met	
405 410 415	
cgc aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag	1296
Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys	
420 425 430	
ggt gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac	1344
Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr	
435 440 445	
aca gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg	1392
Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr	
450 455 460	
gtt ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct	1440
Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro	
465 470 475 480	
agg gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt	1488
Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser	
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agc tcg tga	1497
Ser Ser	

<210> 14
 <211> 498
 <212> PRT
 <213> Aspergillus niger

<400> 14
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Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
35 40 45
Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
50 55 60
Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
65 70 75 80
Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
85 90 95
Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
100 105 110
Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
115 120 125
Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
130 135 140
Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
145 150 155 160
Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
165 170 175
Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
180 185 190
Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
195 200 205
Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
210 215 220
Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
225 230 235 240
Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
245 250 255
Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
260 265 270
Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
275 280 285
Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
290 295 300
Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
305 310 315 320
Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
325 330 335

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
 340 345 350
 Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
 355 360 365
 Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
 370 375 380
 Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
 385 390 395 400
 Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
 405 410 415
 Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
 420 425 430
 Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
 435 440 445
 Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
 450 455 460
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 485 490 495
 Ser Ser

<210> 15
 <211> 3570
 <212> DNA
 <213> *Aspergillus niger*

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 ataaatgaaa gcacgcatgt atcagcctaa tagccgagtg gcgggcatct ctggcggcct 180
 cccgagcagc gtggaatgcg tccaagatcc cgtccgcggg tcgtccttcg gtcggaatga 240
 tgactggagc agcagacgat gtcctgagct gaatgcatgt gatattcaca ttccagggag 300
 aattgtcggc tatttagaac cctctcggct taaaagccct attagactat ggggtgcgctc 360
 aagccactag ccaggatata ccgctgaacg ctccatcacc ttgcagctga agtgcaacat 420
 gggacgggct ttaacttttc gtagatataa gtttaattta tcctctccac acccataggg 480
 tcgtatggtg tcaaccggtg tagtctgcag gatttcacat cgcttcgcca agcgaggcgc 540
 cctaaccggc agcctgcagc ttaccctggt aaccccggtc caccacccc cgagcaatcc 600
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 cgtattcagt taacagtcag tagtcccgtg tcggagattt gttgttctgc aacaattaaa 720
 ggggaccagg gttaaactct ggccccgaa ctgatcggag tttcggccaa tgagagatgt 780
 tgtatacccc cgttcctggc agatggatta attgccggct ccatttgga tccatcaagc 840
 atcatacggg attagaaggg tagttcgtgg gttgatctgc cgtgcaagg gctcaaggct 900
 ctggagtcac gctgaacgca aatattttaag aatcgtcgtc agggacagcg ttctctggat 960
 agtcaagctg tgcttgggac gctgttctgt cgctttgtca aaacataatt cgcagcgatg 1020
 agattatcga cttcgagtct cttcctttcc gtgtctctgc tggggaagct ggccctcggg 1080

ctgtcggctg	cagaatggcg	cactcagtcg	atttacttcc	tattgacgga	tcgggttcggt	1140
aggacggaca	attcgacgac	agctacatgc	gatacgggtg	accaagtacg	ttggtattgc	1200
aggacttcca	tcattcatct	actgacttga	atagatctat	tgtggtggca	gttggcaagg	1260
aatcatcaac	catgtttgtg	atcacttcat	actatccgct	gtgcgcgtgt	ctgactttat	1320
ttgctgcagc	tggattatat	ccagggcatg	ggattcacgg	ccatctggat	ctcgcctatc	1380
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ctgcttcagc	atccttatca	gtgaactcca	agtgccaaacg	ctaactgtac	cagggctacg	1680
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cctcagctac	atcttccctc	ccgacggcat	ccccatcgtc	tacgccggcg	aagaacagca	2460
ctactccggc	ggcaaggtgc	cctacaaccg	cgaagcgacc	tggctttcag	gctacgacac	2520
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cggcgatatt	cccgtgccga	tggcgtcggg	attaccgaga	gttcttctgc	ccgcgtccgt	2940
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ggtcggttac	tgtgacgttg	ccggtgggga	ccactttcga	gtataagttt	attaaggtgg	3060
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gtgggagtgg	ggagacgggtg	gttgatactt	ggaggtagat	gatctgagat	ttctaagtgt	3180
gatgaggggtg	gttttgggtg	atgtagtgtt	gcctttggta	gtgttgggtt	gggttgggtt	3240
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tagccagtgg	gcttgaagaa	aagtctcctg	ggtctctggt	ttgagtaccc	atgttaagat	3420
caagcataaa	aacatgaaat	attgggaaaa	caaagggtat	ttaacaactc	gtgagcatta	3480
gctcctgggt	agaatgcaat	cataacagaa	agtacagcca	gcgctgtgtc	ataaagaagt	3540
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 <212> DNA
 <213> *Aspergillus niger*

<220>
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1	5	10
		15

aag ctg gcc ctc ggg ctg tcg gct gca gaa tgg cgc act cag tcg att	96
Lys Leu Ala Leu Gly Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile	
20 25 30	
tac ttc cta ttg acg gat cgg ttc ggt agg acg gac aat tcg acg aca	144
Tyr Phe Leu Leu Thr Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr	
35 40 45	
gct aca tgc gat acg ggt gac caa atc tat tgt ggt ggc agt tgg caa	192
Ala Thr Cys Asp Thr Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln	
50 55 60	
gga atc atc aac cat ctg gat tat atc cag ggc atg gga ttc acg gcc	240
Gly Ile Ile Asn His Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala	
65 70 75 80	
atc tgg atc tcg cct atc act gaa cag ctg ccc cag gat act gct gat	288
Ile Trp Ile Ser Pro Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp	
85 90 95	
ggt gaa gct tac cat gga tat tgg cag cag aag ata tac gac gtg aac	336
Gly Glu Ala Tyr His Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn	
100 105 110	
tcc aac ttc ggc act gca gat gac ctc aag tcc ctc tca gat gcg ctt	384
Ser Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu	
115 120 125	
cat gcc cgc gga atg tac ctc atg gtg gac gtc gtc cct aac cac atg	432
His Ala Arg Gly Met Tyr Leu Met Val Asp Val Val Pro Asn His Met	
130 135 140	
ggc tac gcc ggc aac ggc aac gat gta gac tac agc gtc ttc gac ccc	480
Gly Tyr Ala Gly Asn Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro	
145 150 155 160	
ttc gat tcc tcc tcc tac ttc cac cca tac tgc ctg atc aca gat tgg	528
Phe Asp Ser Ser Ser Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp	
165 170 175	
gac aac ttg acc atg gtc caa gat tgt tgg gag ggt gac acc atc gta	576
Asp Asn Leu Thr Met Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val	
180 185 190	
tct ctg cca gac cta aac acc acc gaa act gcc gtg aga aca atc tgg	624
Ser Leu Pro Asp Leu Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp	
195 200 205	
tat gac tgg gta gcc gac ctg gta tcc aat tat tca gtc gac gga ctc	672
Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu	
210 215 220	
cgc atc gac agt gtc ctc gaa gtc gaa cca gac ttc ttc ccg ggc tac	720
Arg Ile Asp Ser Val Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr	
225 230 235 240	

cag gaa gca gca ggt gtc tac tgc gtc ggc gaa gtc gac aac ggc aac Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn 245 250 255	768
cct gcc ctc gac tgc cca tac cag aag gtc ctg gac ggc gtc ctc aac Pro Ala Leu Asp Cys Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn 260 265 270	816
tat ccg atc tac tgg caa ctc ctc tac gcc ttc gaa tcc tcc agc ggc Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly 275 280 285	864
agc atc agc aac ctc tac aac atg atc aaa tcc gtc gca agc gac tgc Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys 290 295 300	912
tcc gat ccg aca cta ctc ggc aac ttc atc gaa aac cac gac aat ccc Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro 305 310 315 320	960
cgt ttc gcc tcc tac acc tcc gac tac tcg caa gcc aaa aac gtc ctc Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu 325 330 335	1008
agc tac atc ttc ctc tcc gac ggc atc ccc atc gtc tac gcc ggc gaa Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu 340 345 350	1056
gaa cag cac tac tcc ggc ggc aag gtg ccc tac aac cgc gaa gcg acc Glu Gln His Tyr Ser Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr 355 360 365	1104
tgg ctt tca ggc tac gac acc tcc gca gag ctg tac acc tgg ata gcc Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala 370 375 380	1152
acc acg aac gcg atc cgc aaa cta gcc atc tca gct gac tcg gcc tac Thr Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr 385 390 395 400	1200
att acc tac gcg aat gat gca ttc tac act gac agc aac acc atc gca Ile Thr Tyr Ala Asn Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala 405 410 415	1248
atg cgc aaa ggc acc tca ggg agc caa gtc atc acc gtc ctc tcc aac Met Arg Lys Gly Thr Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn 420 425 430	1296
aaa ggc tcc tca gga agc agc tac acc ctg acc ctc agc gga agc ggc Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly 435 440 445	1344
tac aca tcc ggc acg aag ctg atc gaa gcg tac aca tgc aca tcc gtg Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val 450 455 460	1392

acc	gtg	gac	tcg	agc	ggc	gat	att	ccc	gtg	ccg	atg	gcg	tcg	gga	tta	1440
Thr	Val	Asp	Ser	Ser	Gly	Asp	Ile	Pro	Val	Pro	Met	Ala	Ser	Gly	Leu	
465					470				475					480		

ccg	aga	gtt	ctt	ctg	ccc	gcg	tcc	gtc	gtc	gat	agc	tct	tcg	ctc	tgt	1488
Pro	Arg	Val	Leu	Leu	Pro	Ala	Ser	Val	Val	Asp	Ser	Ser	Ser	Leu	Cys	
			485					490						495		

ggc	ggg	agc	gga	aga	tta	tac	gtc	gag	taa	1518
Gly	Gly	Ser	Gly	Arg	Leu	Tyr	Val	Glu		
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<210> 17
 <211> 505
 <212> PRT
 <213> *Aspergillus niger*

<400> 17															
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Lys	Leu	Ala	Leu	Gly	Leu	Ser	Ala	Ala	Glu	Trp	Arg	Thr	Gln	Ser	Ile
		20					25						30		
Tyr	Phe	Leu	Leu	Thr	Asp	Arg	Phe	Gly	Arg	Thr	Asp	Asn	Ser	Thr	Thr
	35						40					45			
Ala	Thr	Cys	Asp	Thr	Gly	Asp	Gln	Ile	Tyr	Cys	Gly	Gly	Ser	Trp	Gln
	50					55					60				
Gly	Ile	Ile	Asn	His	Leu	Asp	Tyr	Ile	Gln	Gly	Met	Gly	Phe	Thr	Ala
65					70					75					80
Ile	Trp	Ile	Ser	Pro	Ile	Thr	Glu	Gln	Leu	Pro	Gln	Asp	Thr	Ala	Asp
			85						90					95	
Gly	Glu	Ala	Tyr	His	Gly	Tyr	Trp	Gln	Gln	Lys	Ile	Tyr	Asp	Val	Asn
		100						105					110		
Ser	Asn	Phe	Gly	Thr	Ala	Asp	Asp	Leu	Lys	Ser	Leu	Ser	Asp	Ala	Leu
		115					120					125			
His	Ala	Arg	Gly	Met	Tyr	Leu	Met	Val	Asp	Val	Val	Pro	Asn	His	Met
	130					135					140				
Gly	Tyr	Ala	Gly	Asn	Gly	Asn	Asp	Val	Asp	Tyr	Ser	Val	Phe	Asp	Pro
145				150						155					160
Phe	Asp	Ser	Ser	Ser	Tyr	Phe	His	Pro	Tyr	Cys	Leu	Ile	Thr	Asp	Trp
			165						170					175	
Asp	Asn	Leu	Thr	Met	Val	Gln	Asp	Cys	Trp	Glu	Gly	Asp	Thr	Ile	Val
		180						185					190		
Ser	Leu	Pro	Asp	Leu	Asn	Thr	Thr	Glu	Thr	Ala	Val	Arg	Thr	Ile	Trp
		195					200					205			

Tyr Asp Trp Val Ala Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu
 210 215 220
 Arg Ile Asp Ser Val Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr
 225 230 235 240
 Gln Glu Ala Ala Gly Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn
 245 250 255
 Pro Ala Leu Asp Cys Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn
 260 265 270
 Tyr Pro Ile Tyr Trp Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly
 275 280 285
 Ser Ile Ser Asn Leu Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys
 290 295 300
 Ser Asp Pro Thr Leu Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro
 305 310 315 320
 Arg Phe Ala Ser Tyr Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu
 325 330 335
 Ser Tyr Ile Phe Leu Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu
 340 345 350
 Glu Gln His Tyr Ser Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr
 355 360 365
 Trp Leu Ser Gly Tyr Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala
 370 375 380
 Thr Thr Asn Ala Ile Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr
 385 390 395 400
 Ile Thr Tyr Ala Asn Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala
 405 410 415
 Met Arg Lys Gly Thr Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn
 420 425 430
 Lys Gly Ser Ser Gly Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly
 435 440 445
 Tyr Thr Ser Gly Thr Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val
 450 455 460
 Thr Val Asp Ser Ser Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu
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 Pro Arg Val Leu Leu Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys
 485 490 495
 Gly Gly Ser Gly Arg Leu Tyr Val Glu
 500 505

<210> 18
 <211> 2935
 <212> DNA
 <213> *Penicillium chrysogenum*

<400> 18

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Asn Val Ala Asn Leu Gln Thr Phe Ala Gly Met Gly Leu Ile Gly Phe	
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Val Gln Lys Asp Gln Tyr Asp Arg Tyr Met His Met Ser Asn Thr Asn	
355 360 365	
atc atc atc cct cag cgt gca aat gac tat gcg tct ctt gcg ttg tct	1152
Ile Ile Ile Pro Gln Arg Ala Asn Asp Tyr Ala Ser Leu Ala Leu Ser	
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Ser Leu Ile His Ala Leu Tyr Glu Leu Glu Ser Tyr Ala Val Ala Arg	
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Leu Val Thr Lys Glu Ser Lys Pro Pro Met Leu Val Leu Leu Ala Pro	
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Ser Ile Glu Ala Asp Tyr Glu Cys Leu Ile Glu Val Gln Leu Pro Phe	
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Ala Glu Asp Val Arg Ser Tyr Arg Phe Pro Pro Leu Asp Lys Ile Ile	
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Thr Val Ser Gly Lys Val Val Thr Glu His Arg Asn Leu Pro Ser Val	
450 455 460	

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gaa ttc gca cac ccc tca gaa gac atg gtc aag aac tcc aaa tcc cat Glu Phe Ala His Pro Ser Glu Asp Met Val Lys Asn Ser Lys Ser His 530 535 540	1632
ctt gag aaa ttg atg tcc ata gca gat gtc aag aaa gtt cca ccg aag Leu Glu Lys Leu Met Ser Ile Ala Asp Val Lys Lys Val Pro Pro Lys 545 550 555 560	1680
aca aaa ggc cgt aaa cgc caa cgt gaa aca gag aaa cct ctc tca ggt Thr Lys Gly Arg Lys Arg Gln Arg Glu Thr Glu Lys Pro Leu Ser Gly 565 570 575	1728
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tcc acc gag aat gca atc cca gag ttc aag caa aca ctt tcc cgc gcg Ser Thr Glu Asn Ala Ile Pro Glu Phe Lys Gln Thr Leu Ser Arg Ala 595 600 605	1824
gaa aac atc gac gca atc cac gac gct gtg cag cag atg gct aaa atc Glu Asn Ile Asp Ala Ile His Asp Ala Val Gln Gln Met Ala Lys Ile 610 615 620	1872
atc gag agc cag atc aca cac agc ctc ggt cat tca aat tac gac cgt Ile Glu Ser Gln Ile Thr His Ser Leu Gly His Ser Asn Tyr Asp Arg 625 630 635 640	1920
gtt atc gag ggg ctt ggt act atg cgt gaa gaa ctg gtg gac tat gag Val Ile Glu Gly Leu Gly Thr Met Arg Glu Glu Leu Val Asp Tyr Glu 645 650 655	1968
gaa ccg gcg gtg tac aat gac ttt gtg cgt cag ttg aag ggc aag atg Glu Pro Ala Val Tyr Asn Asp Phe Val Arg Gln Leu Lys Gly Lys Met 660 665 670	2016
ttg cgg gag gag ctg ggt ggg gat cgg agg gag ctg tgg tgg ttt gta Leu Arg Glu Glu Leu Gly Gly Asp Arg Arg Glu Leu Trp Trp Phe Val 675 680 685	2064

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 Arg Lys Gly Lys Leu Gly Leu Ile Gly Lys Ser Glu Val Asp Ser Ser
 690 695 700

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<211> 718

<212> PRT

<213> *Penicillium chrysogenum*

<400> 23

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Met Gln Tyr Val Trp Asp Arg Ile Thr Ala Thr Val Ala Thr Gly Arg
 35 40 45

Lys Thr Ala Thr Val Gly Val Val Gly Leu Arg Thr Asp Val Ser Thr
 50 55 60

His Trp Asp Pro Cys Leu Met Phe Gly Thr Gly Thr Ile Asn Asp Leu
 65 70 75 80

Glu Glu Glu Ser Phe Ser Asn Ile Ser Ile Leu Phe Gly Leu Gly Gln
 85 90 95

Val Leu Met Pro Asp Ile Arg Lys Leu Arg Glu Thr Ile Lys Pro Ser
 100 105 110

Asn Thr Asn Arg Gly Asp Ala Ile Ser Ser Ile Val Ile Ala Met Gln
 115 120 125

Met Ile Ile Asp Tyr Thr Lys Lys Asn Lys Tyr Lys Arg Lys Ile Ile
 130 135 140

Leu Val Thr Asn Gly Thr Gly Val Met Ser Asp Asp Asn Ile Glu Gly
 145 150 155 160

Ile Ile Glu Lys Met Lys Glu Val Asn Ile Glu Leu Val Val Met Tyr
 165 170 175

Tyr Gly Val Lys Glu Glu Asp Lys Asp Ser Arg Lys Ala Glu Asn Glu
 180 185 190

Thr Phe Leu Arg Ser Leu Ala Glu Asp Cys Glu Gly Ala Tyr Gly Thr
 195 200 205

Leu Glu Gln Ala Val Ser Glu Leu Asp Ile Pro Arg Ile Lys Val Thr
 210 215 220

Lys Ser Met Pro Ser Phe Lys Gly Asn Leu Thr Leu Gly Asn Pro Glu
 225 230 235 240
 Glu Tyr Asp Thr Ala Met Thr Ile Pro Val Glu Arg Tyr Phe Arg Thr
 245 250 255
 Tyr Val Ala Lys Pro Ile Ser Ala Ser Ser Phe Val Pro Arg Ser Gly
 260 265 270
 Thr Glu Pro Gly Ser Gln Ala Pro Val Lys Gly Asp Ala Glu Gly Asp
 275 280 285
 Ala Leu Ala Ser Val Arg Thr Ser Arg Thr Tyr Gln Ile Thr Asp Glu
 290 295 300
 Ser Ala Pro Gly Gly Lys Ile Asp Val Glu Arg Asp Asp Leu Ala Lys
 305 310 315 320
 Gly Tyr Glu Tyr Gly Arg Thr Ala Val Pro Ile Glu Gln Thr Asp Glu
 325 330 335
 Asn Val Ala Asn Leu Gln Thr Phe Ala Gly Met Gly Leu Ile Gly Phe
 340 345 350
 Val Gln Lys Asp Gln Tyr Asp Arg Tyr Met His Met Ser Asn Thr Asn
 355 360 365
 Ile Ile Ile Pro Gln Arg Ala Asn Asp Tyr Ala Ser Leu Ala Leu Ser
 370 375 380
 Ser Leu Ile His Ala Leu Tyr Glu Leu Glu Ser Tyr Ala Val Ala Arg
 385 390 395 400
 Leu Val Thr Lys Glu Ser Lys Pro Pro Met Leu Val Leu Leu Ala Pro
 405 410 415
 Ser Ile Glu Ala Asp Tyr Glu Cys Leu Ile Glu Val Gln Leu Pro Phe
 420 425 430
 Ala Glu Asp Val Arg Ser Tyr Arg Phe Pro Pro Leu Asp Lys Ile Ile
 435 440 445
 Thr Val Ser Gly Lys Val Val Thr Glu His Arg Asn Leu Pro Ser Val
 450 455 460
 Ala Leu Lys Asp Ala Met Ser Asn Tyr Val Asp Ser Met Asp Phe Val
 465 470 475 480
 Thr Thr Asn Asp Glu Gly Gln Ala Thr Asp Asp Leu Pro Ile Asp Glu
 485 490 495
 Ser Phe Ser Pro Leu Leu His Arg Ile Glu Ser Ala Val Arg Tyr Arg
 500 505 510
 Ala Val His Pro Asn Asp Pro Val Leu Asp Pro Ser Glu Arg Leu Thr
 515 520 525

Glu	Phe	Ala	His	Pro	Ser	Glu	Asp	Met	Val	Lys	Asn	Ser	Lys	Ser	His
530						535					540				
Leu	Glu	Lys	Leu	Met	Ser	Ile	Ala	Asp	Val	Lys	Lys	Val	Pro	Pro	Lys
545					550					555					560
Thr	Lys	Gly	Arg	Lys	Arg	Gln	Arg	Glu	Thr	Glu	Lys	Pro	Leu	Ser	Gly
				565					570					575	
Leu	Asp	Val	Asp	Ala	Leu	Leu	Ser	Leu	Glu	Pro	Lys	Arg	Thr	Lys	Ile
			580					585					590		
Ser	Thr	Glu	Asn	Ala	Ile	Pro	Glu	Phe	Lys	Gln	Thr	Leu	Ser	Arg	Ala
		595					600					605			
Glu	Asn	Ile	Asp	Ala	Ile	His	Asp	Ala	Val	Gln	Gln	Met	Ala	Lys	Ile
610						615					620				
Ile	Glu	Ser	Gln	Ile	Thr	His	Ser	Leu	Gly	His	Ser	Asn	Tyr	Asp	Arg
625					630					635					640
Val	Ile	Glu	Gly	Leu	Gly	Thr	Met	Arg	Glu	Glu	Leu	Val	Asp	Tyr	Glu
				645					650					655	
Glu	Pro	Ala	Val	Tyr	Asn	Asp	Phe	Val	Arg	Gln	Leu	Lys	Gly	Lys	Met
			660					665					670		
Leu	Arg	Glu	Glu	Leu	Gly	Gly	Asp	Arg	Arg	Glu	Leu	Trp	Trp	Phe	Val
		675					680					685			
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	690					695					700				
Ala	Val	Glu	Glu	Gln	Glu	Ala	Gln	Glu	Phe	Leu	Ala	Pro	Asn		
705					710					715					